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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/647,978A

DATE: 06/28/2002

TIME: 11:05:41

Input Set : A:\57961.app

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3 <110> APPLICANT: Warner-Lambert Company
 5 <120> TITLE OF INVENTION: Gene Encoding Syntaxin Interacting Protein
 7 <130> FILE REFERENCE: 09/647,978
 9 <140> CURRENT APPLICATION NUMBER: 09/647,978A
 10 <141> CURRENT FILING DATE: 2000-10-06
 12 <150> PRIOR APPLICATION NUMBER: PCT/US99/08568
 13 <151> PRIOR FILING DATE: 1999-04-19
 15 <150> PRIOR APPLICATION NUMBER: 60/082,454
 16 <151> PRIOR FILING DATE: 1998-04-20
 18 <160> NUMBER OF SEQ ID NOS: 6
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1674
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Mouse
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 30 aggaatgaag gaccgctggt gtatatcat gaagtcattc ctggagggtga ctgttacaag 180
 31 gatggacgtt tgaagccagg agatcaactt gtctcaataa acaaggaatc tatgattggt 240
 32 gtatcatttg aagaagcaaa aagcataatt accagagcca agttgaggtc agaattctcc 300
 33 tgggagatag cattcatcag acaaaagtct tactgtggcc atccaggaaa tatttgctgt 360
 34 ccatcccccac aagtgtcaga agactgtgga cctcaaacct caacatttac tcttctttcc 420
 35 tctcctctctg aaactact tccaaagact tcatccactc cccagactca ggactccact 480
 36 ttcccttctt gtaagcaat tcagacaaaa cctgaacacg ataaaacaga acatagtcca 540
 37 attacttctt tggacaacag cctgcagat acatctaatt cagacattgc tccagcctgg 600
 38 actgatgatg attctggacc acaaggaaag atttccctaa atccttctgt tcgccttaag 660
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 40 gaagccctga gagagcaagt ccaggccgac tcaaagggga ctgtgtcttt tggagatttc 780
 41 gtccagggtt ccagaagttt gttttgcttg cagtggatg aagtaaattg tgggtgccat 840
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 43 gtgggaaaaac ttagacaaga aagaaacgct gctctagagg aacggaatgt gcttaaggag 960
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 46 gaagctgcac agcggcaggc acacgggatg gaaattgatt atgaagaggg gatccgtctg 1140
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61 <213> ORGANISM: Mouse
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68           20           25           30
70 Leu Lys Ile Leu Gly Gly Ile Asn Arg Asn Glu Gly Pro Leu Val Tyr
71           35           40           45
73 Ile His Glu Val Ile Pro Gly Gly Asp Cys Tyr Lys Asp Gly Arg Leu
74           50           55           60
76 Lys Pro Gly Asp Gln Leu Val Ser Ile Asn Lys Glu Ser Met Ile Gly
77   65           70           75           80
79 Val Ser Phe Glu Glu Ala Lys Ser Ile Ile Thr Arg Ala Lys Leu Arg
80           85           90           95
82 Ser Glu Ser Pro Trp Glu Ile Ala Phe Ile Arg Gln Lys Ser Tyr Cys
83           100          105          110
85 Gly His Pro Gly Asn Ile Cys Cys Pro Ser Pro Gln Val Ser Glu Asp
86           115          120          125
88 Cys Gly Pro Gln Thr Ser Thr Phe Thr Leu Leu Ser Ser Pro Ser Glu
89           130          135          140
91 Thr Leu Leu Pro Lys Thr Ser Ser Thr Pro Gln Thr Gln Asp Ser Thr
92 145           150           155           160
94 Phe Pro Ser Cys Lys Ala Ile Gln Thr Lys Pro Glu His Asp Lys Thr
95           165           170           175
97 Glu His Ser Pro Ile Thr Ser Leu Asp Asn Ser Pro Ala Asp Thr Ser
98           180          185          190
100 Asn Ala Asp Ile Ala Pro Ala Trp Thr Asp Asp Asp Ser Gly Pro Gln
101           195          200          205
103 Gly Lys Ile Ser Leu Asn Pro Ser Val Arg Leu Lys Ala Glu Lys Leu
104           210          215          220
106 Glu Met Ala Leu Asn Tyr Leu Gly Ile Gln Pro Thr Lys Glu Gln Arg
107 225           230           235           240
109 Glu Ala Leu Arg Glu Gln Val Gln Ala Asp Ser Lys Gly Thr Val Ser
110           245          250          255
112 Phe Gly Asp Phe Val Gln Val Ala Arg Ser Leu Phe Cys Leu Gln Leu
113           260          265          270
115 Asp Glu Val Asn Val Gly Val His Glu Ile Pro Ser Ile Leu Asp Ser
116           275          280          285
118 Gln Leu Leu Pro Cys Asp Ser Leu Glu Ala Asp Glu Val Gly Lys Leu
119           290          295          300
121 Arg Gln Glu Arg Asn Ala Ala Leu Glu Glu Arg Asn Val Leu Lys Glu
122 305           310          315          320
124 Lys Leu Leu Glu Ser Glu Lys His Arg Lys Gln Leu Ile Glu Glu Leu
125           325          330          335
127 Gln Asn Val Lys Gln Glu Ala Lys Ala Val Ala Glu Glu Thr Arg Ala

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128          340          345          350
130 Leu Arg Ser Arg Ile His Leu Ala Glu Ala Ala Gln Arg Gln Ala His
131          355          360          365
133 Gly Met Glu Met Asp Tyr Glu Val Ile Arg Leu Leu Glu Ala Glu
134          370          375          380
136 Val Ser Glu Leu Lys Ala Gln Leu Ala Asp Tyr Ser Asp Gln Asn Lys
137 385          390          395          400
139 Glu Ser Val Gln Asp Leu Arg Lys Arg Val Thr Val Leu Asp Cys Gln
140          405          410          415
142 Leu Arg Lys Ser Glu Met Ala Arg Lys Ala Phe Lys Ala Ser Thr Glu
143          420          425          430
145 Arg Leu Leu Gly Phe Ile Glu Ala Ile Gln Glu Val Leu Leu Asp Ser
146          435          440          445
148 Ser Ala Pro Leu Ser Thr Leu Ser Glu Arg Arg Ala Val Leu Ala Ser
149          450          455          460
151 Gln Thr Ser Leu Pro Leu Leu Ala Arg Asn Gly Arg Ser Phe Pro Ala
152 465          470          475          480
154 Thr Leu Leu Leu Glu Ser Lys Glu Leu Val Arg Ser Val Arg Ala Ile
155          485          490          495
157 Leu Asp Met Asp Cys Leu Pro Tyr Gly Trp Glu Glu Ala Tyr Thr Ala
158          500          505          510
160 Asp Gly Ile Lys Tyr Phe Ile Asn His Val Thr Gln Thr Thr Ser Trp
161          515          520          525
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166 Glu Glu Asp Cys Pro Arg Glu Leu Thr Asp Pro Lys Ser
167 545          550          555
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171 <211> LENGTH: 2075
172 <212> TYPE: DNA
173 <213> ORGANISM: Human
175 <400> SEQUENCE: 3
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177 agttcctgga ataattattag tcagagtaat ataggatctg caggaagtgt ctcaagatag 120
178 ttggaaaaga agaatttcta gactcttcat caagatcttc atttatacag ctgttaaatac 180
179 caaggctact ttggtgaaag catgaataaa aatacatcta ctgtagtatc acccagtcta 240
180 cttgaaaagg atcctgcctt tcagatgatt acaattgcc aaggaaacagg ccttggcctg 300
181 aaggtagtag gaggaattaa ccggaatgaa ggcccattgg tatatatcca ggaaattatt 360
182 cctggaggag actgttataa ggatggtcgt ttgaagccag gagatcaact tgtctcagtc 420
183 aacaaggaat ctatgattgg tgtatcattt gaagaagcaa aaagcataat taccagagcc 480
184 aagttgaggt tagaatctgc ttgggagata gcattcataa gacaaaaatc cgacaacatt 540
185 cagccagaaa atctgtcatg tacatcactt atagaagctt caggagaata tggacctcaa 600
186 gcctcaacat taagtctttt ttcttctcct cctgaaatac taatcccaaa gacctcatcc 660
187 actcccaaaa caaataatga cattttatct tcttgtaga taaaaactgg atacaacaaa 720
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189 gcttctgcct ggactgaaaa ttatgggcta caagaaaaga tctccctaaa tccctctgtt 840
190 cgctttaagg cagagaaact ggaaatggct ctaaattatc ttggtattca gccacaaaag 900
191 gaacaacacc aagccctgag acagcaagta caagcagact caaaagggac agtgtctttt 960
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193 ggtgcacatg aaatttccaa tatattagat tcacagcttc ttccttgtga ttcttcagaa 1080
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195 cttaaaggaaa aattattgga atcagataag caaaggaaac aattgacaga agagctccag 1200
196 aatgtgaaac aagaagccaa agctgtagtt gaagaaacaa gagccctgcg tagtcggatt 1260
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201 gtagaggcta ttcaagaagt attttctgat aattctactc ctttatcaaa ttttaagtga 1560
202 agaagagctg tgtagcttc tcagacttcc ctcacaccac tgggaaggaa tggacgtagc 1620
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204 gatattgatt gtttacctta tgggtgggag gaagcttaca cagcagatgg aatcaagtac 1740
205 ttcatcaatc atgtaacaca gactacatcc tggatccatc ccgtgatgag tgtcctgaat 1800
206 ctatctcgct cagaggagaa tgaagaggat tgctctagag aactcccaa ccagaaaagt 1860
207 tgatggtttt ccttaggaag tggagctaca tggatgatgt gagcagagac gcataacatc 1920
208 caattctgag atgaaacagt ctaaaatagg agtaaagcat gcaactactg ttgaagtgtg 1980
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213 <210> SEQ ID NO: 4

214 <211> LENGTH: 1662

215 <212> TYPE: DNA

216 <213> ORGANISM: Human

218 <400> SEQUENCE: 4

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221 cggaatgaag gccatttgt atatatccag gaaattattc ctggaggaga ctgttataag 180
222 gatggctggt tgaagccagg agatcaactt gtctcagtc acaaggaatc tatgattggt 240
223 gtatcatttg aagaagcaaa aagcataatt accagagcca agttgagggt agaactctgt 300
224 tgggagatag cattcataag acaaaaatcc gacaacattc agccagaaaa tctgtcatgt 360
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226 tcttctcttc ctgaaatact aatcccaaag acctcatcca ctcccaaac aaataatgac 480
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231 cagcaagtac aagcagactc aaaagggaca gtgtcttttg gagattttgt ccaggttgcc 780
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251 <212> TYPE: PRT
252 <213> ORGANISM: Human
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262 35 40 45
264 Ile Gln Glu Ile Ile Pro Gly Gly Asp Cys Tyr Lys Asp Gly Arg Leu
265 50 55 60
267 Lys Pro Gly Asp Gln Leu Val Ser Val Asn Lys Glu Ser Met Ile Gly
268 65 70 75 80
270 Val Ser Phe Glu Glu Ala Lys Ser Ile Ile Thr Arg Ala Lys Leu Arg
271 85 90 95
273 Leu Glu Ser Ala Trp Glu Ile Ala Phe Ile Arg Gln Lys Ser Asp Asn
274 100 105 110
276 Ile Gln Pro Glu Asn Leu Ser Cys Thr Ser Leu Ile Glu Ala Ser Gly
277 115 120 125
279 Glu Tyr Gly Pro Gln Ala Ser Thr Leu Ser Leu Phe Ser Ser Pro Pro
280 130 135 140
282 Glu Ile Leu Ile Pro Lys Thr Ser Ser Thr Pro Lys Thr Asn Asn Asp
283 145 150 155 160
285 Ile Leu Ser Ser Cys Glu Ile Lys Thr Gly Tyr Asn Lys Thr Val Gln
286 165 170 175
288 Ile Pro Ile Thr Ser Glu Asn Ser Thr Val Gly Leu Ser Asn Thr Asp
289 180 185 190
291 Val Ala Ser Ala Trp Thr Glu Asn Tyr Gly Leu Gln Glu Lys Ile Ser
292 195 200 205
294 Leu Asn Pro Ser Val Arg Phe Lys Ala Glu Lys Leu Glu Met Ala Leu
295 210 215 220
297 Asn Tyr Leu Gly Ile Gln Pro Thr Lys Glu Gln His Gln Ala Leu Arg
298 225 230 235 240
300 Gln Gln Val Gln Ala Asp Ser Lys Gly Thr Val Ser Phe Gly Asp Phe
301 245 250 255
303 Val Gln Val Ala Arg Asn Leu Phe Cys Leu Gln Leu Asp Glu Val Asn
304 260 265 270
306 Val Gly Ala His Glu Ile Ser Asn Ile Leu Asp Ser Gln Leu Leu Pro
307 275 280 285
309 Cys Asp Ser Ser Glu Ala Asp Glu Met Glu Arg Leu Lys Cys Glu Arg
310 290 295 300
312 Asp Asp Ala Leu Lys Glu Val Asn Thr Leu Lys Glu Lys Leu Leu Glu
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VERIFICATION SUMMARY

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